

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: DE LEON, F. Abel Ponce
CIUFO, Stacy
ROBL, James M.
AMBADY, Sakthikumar
SMYTH, JR., J. Robert

(ii) TITLE OF INVENTION: Z-CHROMOSOMAL MARKERS DERIVED FROM
CHICKEN (GALLUS DOMESTICUS) AND USE THEREOF IN CHROMOSOMAL
MAPPING

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/034,410
(B) FILING DATE: 02-JAN-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Teskin, Robin L.
(B) REGISTRATION NUMBER: 35,030
(C) REFERENCE/DOCKET NUMBER: 002076-001

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCACTTTC CCTAATATTG TTGTGTTCT TGTTGTTGA CCTGTAATGC AGTTCTGAGT 60
TTTGGAAAGG AACTAATTAA GACCAGAGGA GAGATAATTG TCTTTATCA AAAAACAAAC 120
AAACAAACAA AAAAACGAAT TCTTACCACT TTACAAAAAT TTTCCATTGTT GAAGGCCAGT 180
ACAGCCATAG CATTCATCTA CTTTTTGCTT TGGAT 215

(2) INFORMATION FOR SEQ ID NO:2:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCAGGTGG CCTGTAGTAG ACAACAAACAA CAATGGGGTG CCCTTGTTG CCTTAGTCTC 60
TAACTCGCAC CCACACACAC TTTCAAGTTG CTTGTGGCCA TTCTTCAGGG ACAGTTCTTC 120
ACAATCTATT CCTTTCTGA TGTAGAAGGC GTCACCTCCT CCCCTCCTGC CTCGTTGTC 180
CCTTCTAAC TGCAGGTATT AGTATTGATA GCTAAGGTCA AGTCATGGGA ACCATCTCAC 240
CAGGTTTCAG TGTTGGCAAC TATGTTATGC TTTCTTAGGA GCATGGTGGT TCCAACTCTT 300
CCCTGCTTAT TTCCCAAGCT GTGTGTGATG GTAGGATAGC ATTCAAGTGG GAGGAGCCTA 360
TCGGCTTTT GGAGGTACTC CTAAATCCCT GATATTCCCC TGATTCCCGT ACTTCTTCCT 420
TGCCAAGGGC CCGCCAATGC ATAGTTCAAT TTCTCATGCA GACGCTAAGG AAAGGTGGAC 480
CC 482

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCGTATGT ATTTTTTAC ATAGGATAGA AAATGGCCAA TAGGAAATAA GACAGTACAG	60
CTACTAAGAA AGAAACACAA TTACACACAC ACACACACAC ACACACACAC ACACATTGA	120
AAAACGCGCT GCACAGCAGT GTGGGTATT TTTCACAAGA GAGACACACT CTACAGTACA	180
CAGCCAGCTC TACCTTGTCG CACAGTCTCA GTGTGTGTTT GCCAACAGGA CGCGGTTCAC	240
AGGGAGATAT TGTCCCTTTG TGTGTGTGGA GACACAGAGA CAGAG	285

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCCCCTGG AGGAAGGGCA ATGGCAACCC ACTCCAGTAT TCTTGCCCTGA AGAATACCAT	60
GGTCAGTTT GCCTCCTGGG CTATAGTCCA TGGGGTTGCA AAGAGTCAGG CATGACTGAG	120
CGACTCTCTC TCTCTCTCTC TCTCTCTCTC ACACACACAC ACACACACAC ACACACGGCG	180
TCTCTCTCTC TCTCTATACA TATAGGCTGT GTGTCTCGCT ATTCTCACAT GAGGGAAACT	240
CATATCTAGC ACGTGGCACA AATATTGTTT GTGGCTCTCA CAAAAGACAT GTGGGCGCAC	300
AAAGGTCCCC CCCCGGTGGA TACANCGCCT TGGTTTTTA TAACCCAAGC CTGTG	355

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCACATAT GTAAACTAGG GAATTGCATA ATAAGATTAA ATGTAGGTGT AGAACGTGGC 60
ATGAAGGAAG GTAGAATTAG GTGGTACCTA TCTCTTCTGA AACAAACTGA GAATCCTACT 120
ACCAATCAAC ATATTCTACA TACCACACAC ACATTTTTTC TCGAGTAAAA TATAAACTAA 180
TGAGAAACTT CCCTAG 196

(2) INFORMATION FOR SEQ ID NO:6:

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con
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCCAAGC AACACATAGN CAGACAATCA CACACACACA CACACACACA CACACACACA 60
CACACACACA CACATCCTCT CCCACAAATA CATCCGAGA GGGGGGAGAG ACACTCTCTC 120
TCCCTCTCTA TAGGGGAGAC CGGGAGAGCT GGCTCTGTTG TCTCTCTACA CGGGACATAC 180
AGTGGAGCAC ATCTCACACT TGTGTCTTG TCTCTCTACA CGGGACATAC AGTGGAGCAC 240
ATCTCACACT TGTGTCTCTA TCTCTCCCTG TCCCTGTTGA TCCATCTCTC TTCACACATC 300
TCTCCAGATC TTAGCGCTAG AGTCTCCTGT CTTCTCTCTG CGCAATTGT GTGATAGAGA 360
CACCTGATAT GTTGTGTGGG GGAGACATCT GTGTGTCTCT GTGTCATCCC AGAGGATTT 420
TCTCTCCAC ACTTAGAGGC CTTCTCAAGA GATGGGAGGT TTTAATGGGG TGTG 474

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCATTCTT CTGTTCCCA TTCTAATGGG AATTCTCCAC ACACACACAC ACACACACAC 60
ACACACACAT CTTCTTCCCC TTACATGGAA AAAAATCCTC CACACCCCTG GACACTGATT 120
ACTCTCCCTC TTCCCAGAGA GAGATC 146

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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CBM (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATCCCCTAG AGAAGGGAAT GGCTACTCAC TCCAGTATTG TTGCCTGGAG AATTCCGTGG 60
TCAGAGGAGC CTGGAAGGCT ATAATCCATA GAGTCGCAAG AGTCAGACAG GACTGAGTGA 120
CTAACACACA CATGCACACA CACACACACA CACACACACA CTTGCTCTAG GGAGAGGCAT 180
AGAGATGTA TCTCTCCTAA AATGGGGTG GCGATGGCCC CTGCGGCCAA GTAATGCCA 240
CACATGCGTA TTCCCCTTAA GATTGGGTTA GGCCCTCCCTT ATGAGGAGAG ACCAGGGAGA 300
GAATGGGCTC TCTCTCTCTC TCACTCCCCA ACCGAGTAAG TGGTAAAAAA GTTTTCCTG 360
GATTACAATT TTGGTGTAC AGAATTGGAA AAAAATATTG TTGGGGCTCC CCCCTCAGTT 420
TA 422

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGCAAAAA CACCCCCACA AGTTATGAAA ACAACGGCTT AATATAGTAA TGTGTGTGTG 60
TGTGTGTGTG TGTTGCACAC CACAGTTTC TCTGATACTC AAACCTCTCT CTTTCTCTAC 120

AGGGGCCCCC CATAACACAG CGGCTGAGAT GTGTGACGGG AAGGCGTGGC CTTTTACACA 180
TTTGTGGTAT GGTCTGCCAA GGCCCCCTAT TGCCCCCCAC AACTACGGAG ATACACTAGG 240
GGCGACCCGC AGCGCGCGA CCCCCAGGTG GGGCCCCGAG 280

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTTAGGAGG TTCTCTCGAG TAAGCTTTT GGATTCTTT GGTTCCAAG CATCACATGG 60
TACAGGCAGT CACACACACA CACATACACA CACACACACA CACACACACA CACTCCTCTC 120
CCCACAAATAC ATACCGAGAG GGGGGAGAGA CACTCTCTCT CCCTCTCTAT AGGGGGAGCC 180
CCACAGAGCT GGCTCTGTTG TCTCTCTCCA CCGGACATAC AGTGGAGCAC ATCTCACACT 240
TCTGTCTCTA TCTCTCCCTG CCCCTGTGAC ATCCATCTCT CTTCACACAA TCTCACCCAG 300
GATCTTAGCG CTAGAGACCC CCTGTCCTTC TTCTCCTGGG GAAATTTTT GTGGATAAGA 360
GACACCCGAT ATATTGGTGT GGGGGAGAAC ATCTTGAG GTCTCTGTTG TGCCATCCCA 420
ACAGGAATT TTATCTCCCC CACAATTAGA GGCCCCTCCT CAAGAGTGTG TGAGGGTT 478

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCACAGAT GTATGTATTT TTTTACATAG GATAGAAAAT GGACAATAGG AAATAAGACA 60
GTACAGCTAC TAAGAAAGAA CCCACATTAA CACACACACA CACACACACA CACACACACA 120

AGTGTTTAAT CCGCTGCACA GCATTGTGGA CATTTCACCA CAAGAGAGAC ACACCTCTACA 180

GTTTGCGCCC AGCTCTAG 198

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATCATTCTT CTGTTTCCCA TTCTAATGGA ATTCTCCACA CACACACACA CACACACACA 60

CACACACTCT TCTTTCTCCT GACATGGAAA AATCTCCCCC ACACCCCGGG ACACTGATT 120

CTCTCCCTCT CCCCAACACT GTGAGCAAGA GGAGTTTATT TTGTGTGTGT CACTCTTCCA 180

GGGAGAGAGA GATC 194

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTAGGCATCG GTTGGGAGGT GGTGAGTAAT TACTTGTCTG ACATTAGTCC TGTAACATTG 60

GGTGTGTGTG TGTGTGTGTG TGTGTATTCC CCTTGGGAAT TGGTTTCTC AACACAAAGT 120

TCTTCTTTTT TTTTTTCTC CCCCTTTTC TTCTGAAAAT AAGTACTTGG GGGGTTCCG 180

CCCCCCCGG TAAATAAAAT 200

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTAGTGGCTC CCAAGCAACA CATAGCCAGA CAACACACAC ACACACACAC ACACACACAC	60
ACACACACAC ACACACACTC CTCTCCCCAC AATACATCCC GAGAGGGGGG AGAGACACTC	120
TCTCTCCCTC TCTATAGCGG GAGCCCCACA GAGCTGGCTC TGCTGTCTCT CTACACCGGA	180
CATACAGTGG AGCACATCTC ACATTCTGTG CTCTATCTCT CCCTGCCCT GGTGACATAC	240
ATCTCTCTTC ACACATCTCA CCAGGTCTGA GCGCTAGAGT CTCCTGTCTT CTCTCTGC	300
AATATTTGTG ATAGAGACAT CTGATATATT GTGTGTGGGA GACATTTGT GAGTCTCTGT	360
GTGCATCCA GAGGATTTT ATCTCCCCAC ACTAG	395

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCCATGAA AACTTCCGA GTTGTATTGT CTAGGTGAAA ACACACACAA ACACACACAC	60
ACACACACAC ACACAACAGG GAGATGAGTC TTGCAAGAGA ATAGGGAGA GTTATGTCAC	120
CAAGTCTGGT GAGGTATATA GCGTATAGGG AGCCAACATG TCAGACATCT GATGTGCTAA	180
GATTAACATT TTATTTTATT TAATGTGTGA GATCTCATAT AGCGGCTCTT CTTATATATG	240
ACGTCTCGCA ATGTCTCTTT ATGTGTGTTA TTCTCTGAGC CCCTGGGAGA TATCTGTCA	300
CAGAGAGAAG AGACATACAC ATACAGGGGT TATATATTTT CTCCCTGTGT GTGGAGATGG	360
AGGGTATTTT GGACAAGCTC AACACTCATT GGCTCCAGA GAGAGAAAAG GAGCAACTGT	420
TGCACCCGGG GCTCTGTAGC TGGGATC	447

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAATTGGGTA CATCTACCTG GTACCCCCACC CGGGTGGAAA ATCGCATGGG CCCGCAGGGGG 60
TTCTAGGAAG TACTCTCGAG AAGCTTTGG GTTCTTGAG TCCCAAGCAG CACATGGACA 120
GGCAATCACA CACACACACA CACACACACA CACACACACA CTCCTCTCCC 180
CACAATACAT CCCGAGAGGG GGGAGAGTCA CTCTCTCTCC CTCTCTATAG GGGGCGCCCC 240
TAAGAGCTGG CTCTGTTGTC TATCTACACC GCACATACAA TGGAGCACAA CTCACACTAG 300

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCAAAGCA TGGAGGTCAT GCCAGGCCTT GAACAAAATG GTAGAGAGTG ATTCTATGAC 60
TGACTAAGAC CTCATGCAAC AACAAAGTAA GAGTCACAAC TGCAAAACAGA AGTACAACCTT 120
AGCAAATCCT ATTTTCAGGA AACACTAAAC CGTAATACTT GCACGATTT TTCTTTAATA 180
CAGTAATAAT TCTTTTAGAA TTTGGATATA TCTTTAAGA TACATATTTG TCTAAATACC 240
AAGGCAGGAT ATGAGCATAA AATAGCTAAG GTTAGCTATG GTGTTATATT TAAGAAGACC 300
ACAGAGCAAT AGGAGCATAAC TTTTCTTGGG GTAGAAGGGG CCCTTAAAGG TCACCTAG 358

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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CTAGCCACAT CCTATAACTC CACTCCACCT TTAATCCTGA TTTCTGTGTC TCTTCTCTAA	60
CCTCTATGGC CTTTCTCTAA AGTTCCCCAA TATCAACAAT CCTTTTCCCC ACTGGGACCT	120
CCAGTTTATT GATTCTACCA TGTCACTATC CATGGTCAAC CACTTGTGGT ATTATAGGAT	180
GTCGC GTGTG TG GTGTG TG TG TG GCATG TG TG TG GCT TGGGTGTCAG AGAGTTCAA	240
TCTGGGGGAC CTATGGTTTG TAAAC AACAG GTCTCTTGCC AAGGAAGAT	289

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTAGCGCTCG TGCCCCTGCA GTTCGACACT CAGTGGCTCC TCCACACACA CACACACACA	60
CACATCAATA TATATATAGA TAGATAGATA GATAGAGGAG CAATATAAGT GGCTTCTCTA	120
TTTCCAGCAT GTTTGAAGA GCATAAACTC AACAGAGTAT ATATAATCT GATGTGACCC	180
ATGTCATCTG CTACAGCATG AGAGGGGGTA GTGATC	216